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## Entry Information

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## General information

 Entry name **O88927**

 Accession number **O88927**, [O88924](#), [O88928](#), [O88929](#), [O88926](#), [O88925](#)

Created TrEMBLrel. 05, 1-JAN-1998

Sequence update TrEMBLrel. 05, 1-JAN-1998

Annotation update TrEMBLrel. 25, 1-SEP-2003

## Description and origin of the Protein

Description Calcium-independent alpha-latrotoxin receptor 3 precursor (

Organism source Rattus norvegicus (Rat).

Taxonomy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Muridae; Murinae; Rattus.

 NCBI TaxID [10116](#)

## References

- [1] Sugita,S., Ichtchenko,K., Khvotchev,M., Suedhof,T.C., **alpha-Latrotoxin receptor CIRL/latrophilin 1 (CL1) def linked receptors. G-protein coupling not required for tr** (1998) *J. Biol. Chem.* **273**:32715-32724

Position SEQUENCE FROM N.A.

 Medline [99047651](#)

 PubMed [9830014](#)

## Comments

### FUNCTION

 PERFORMS A GENERAL AND UBIQUITOUS FUNCTIO  
 SIGNALING.

### SUBUNIT

 HETERODIMER OF A 120 AND A 85 KDA SUBUNITS  
 PROTEOLYTIC CLEAVAGE OF THE PRECURSOR.

### SUBCELLULAR LOCATION

INTEGRAL MEMBRANE PROTEIN.

### ALTERNATIVE PRODUCTS

 Event=Alternative splicing; Named isoforms=6; Nam  
 Name=CL3AA; IsoId=O88927-2; Sequence=VSP\_0  
 Sequence=VSP\_050431, VSP\_050432, VSP\_050433  
 Sequence=VSP\_050431, VSP\_050434, VSP\_050435  
 Sequence=VSP\_050432, VSP\_050433; Name=CL3B  
 VSP\_050435;

### TISSUE SPECIFICITY

BRAIN.

**PTM** CLEAVED INTO A 120 KDA HYDROPHILIC GLYCOSY  
LEAST PART OF ALPHA-LATROTOXIN-BINDING SITE  
REMAIN STILL TIGHTLY BOUND TO EACH OTHER AF

**SIMILARITY** BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RE

**SIMILARITY** SOME, TO NEURONAL OLFACTOMEDIN-RELATED ER

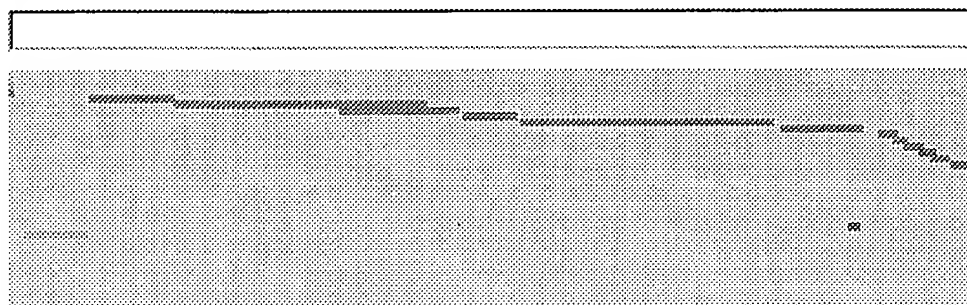
## Database cross-references

**EMBL** [AF081157](#); [AAC62663.1](#); -.  
[AF081154](#); [AAC62660.1](#); -.  
[AF081158](#); [AAC62664.1](#); -.  
[AF081159](#); [AAC62665.1](#); -.  
[AF081156](#); [AAC62662.1](#); -.  
[AF081155](#); [AAC62661.1](#); -.  
**PIR** [T17198](#); T17198.  
**GO** [GO:0016021](#); C:integral to membrane; IEA.  
[GO:0004930](#); F:G-protein coupled receptor activity; IEA.  
[GO:0005529](#); F:sugar binding; IEA.  
[GO:0007218](#); P:neuropeptide signaling pathway; IEA.  
**InterPro** [IPR000922](#); Gal\_lectin.  
[IPR000832](#); GPCR\_secretin.  
[IPR001879](#); hormn\_receptor.  
[IPR003334](#); Latrophilin.  
[IPR003112](#); Olfac\_like.  
[IPR000203](#); PKD\_cys\_rich.  
**Pfam** [PF00002](#); 7tm\_2; 1.  
[PF02140](#); Gal\_Lectin; 1.  
[PF01825](#); GPS; 1.  
[PF02793](#); HRM; 1.  
[PF02354](#); Latrophilin; 1.  
[PF02191](#); OLF; 1.  
**PRINTS** [PR00249](#); GPCRSECRETIN.  
**ProDom** [PD005612](#); Gal\_lectin; 1.  
**SMART** [SM00303](#); GPS; 1.  
[SM00284](#); OLF; 1.  
[PS50221](#); GPS; 1.  
**PROSITE** [PS50227](#); G\_PROTEIN\_RECEP\_F2\_3; 1.  
[PS50261](#); G\_PROTEIN\_RECEP\_F2\_4; 1.  
[PS50228](#); SUEL\_LLECTIN; 1.

## Keywords

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Alter

## Features



Key	Begin	End	Length	Description
<u>SIGNAL</u>			0	POTENTIAL.
<u>CHAIN</u>			0	CALCIUM-INDEPENDENT ALPHA
<u>DOMAIN</u>			0	EXTRACELLULAR (POTENTIAL).
<u>DOMAIN</u>	88	179	92	CYS-RICH, LECTIN-LIKE.
<u>DOMAIN</u>	180	457	278	OLFACTOMEDIN-LIKE.
<u>DOMAIN</u>	361	491	131	PRO-RICH.
<u>DOMAIN</u>	496	556	61	SER/THR-RICH.
<u>DOMAIN</u>	559	835	277	BAI.
<u>DOMAIN</u>	844	933	90	CYS-RICH.
<u>TRANSMEM</u>	949	969	21	POTENTIAL.
<u>DOMAIN</u>	970	977	8	CYTOPLASMIC (POTENTIAL).
<u>TRANSMEM</u>	978	998	21	POTENTIAL.
<u>DOMAIN</u>	999	1006	8	EXTRACELLULAR (POTENTIAL).
<u>TRANSMEM</u>	1007	1027	21	POTENTIAL.
<u>DOMAIN</u>	1028	1048	21	CYTOPLASMIC (POTENTIAL).
<u>TRANSMEM</u>	1049	1069	21	POTENTIAL.
<u>DOMAIN</u>	1070	1087	18	EXTRACELLULAR (POTENTIAL).
<u>TRANSMEM</u>	1088	1108	21	POTENTIAL.
<u>DOMAIN</u>	1109	1132	24	CYTOPLASMIC (POTENTIAL).
<u>TRANSMEM</u>	1133	1153	21	POTENTIAL.
<u>DOMAIN</u>	1154	1159	6	EXTRACELLULAR (POTENTIAL).
<u>TRANSMEM</u>	1160	1180	21	POTENTIAL.
<u>DOMAIN</u>	1181	1527	347	CYTOPLASMIC (POTENTIAL).
<u>DOMAIN</u>	1460	1463	4	POLY-ALA.
<u>SITE</u>	922	923	2	CLEAVAGE (POTENTIAL).
<u>VARSP LIC</u>	19	86	68	Missing (in isoform CL3AA, isofo

<u>VARSP LIC</u>	1263	1298	36	GLLNNARDTSVMDTLP LN GNHGN YRETS MG VK LN IAY QIGASEQCQG CL3AB). /FTId=VSP_050432.
<u>VARSP LIC</u>	1299	1527	229	Missing (in isoform CL3BB and i
<u>VARSP LIC</u>	1262	1341	80	EGLLNNARDTSVMDTLP LN GNHGH DRGYNHNETALEKKILKELTSNYIP GTMANHLM SNALLRPHGTNNPYN MYNAQEPYRETS MG VK LN IAY QIG isoform CL3BC). /FTId=VSP_05
<u>VARSP LIC</u>	1342	1527	186	Missing (in isoform CL3AC and i

## Sequence information

Length: **1527 aa**, molecular weight: **169779 Da**, CRC64 checksum: **A0F1FFC2**

MCPPQLFILM MLLAPVVHGG KHNERHPALA APLRHAHSP GGPLPPRHLL QQPAAERS  
 HRGQGPRTA RGVRGPGAPG AQIAAQAFSR APIPMVVRRL ELSCESYPIE LRCPGTDV  
 IESANYGRD DKICDSDPAQ MENIRCYLPD AYKIMSQR CN NRTQCAVVAG PDVFPDPC  
 TYKYLEVQYE CVPYKVEQKV FLCPGLLKGV YQSEHLFESD HQSGAWCKDP LQASDKIY  
 PWTPIYRTDTL TEYSSKDDFI AGRPTTTYKL PHRVDGTGFV VYDGA LF FNK ERTNRIVK  
 LRTRIKSGEA IIANANYHDT SPYRWGKSD IDLAVDENG L WVIYATEQNN GKIVISQL  
 YTLRIEGTWD TAYDKRSASN AFMICGILYV VKSVYEDDDN EATGNKIDYI YNTDQSKD  
 VDVFPFNSYQ YIAAVDYNPR DNLLYVWNNY HVVKYSLDFG PLDSRSGPVH HGQVSYIS  
 IHLSDLERP PVRGISTTGP LGMGSTTTST TLRTTTWNLG RSTTPSLPGR RNRSTSTP  
 AIEVLDVTTH LPSAASQIPA MEESCEAVEA REIMWFKTRQ GQVAKQSCPA GTIGVSTY  
 LAPDGIWDPQ GPDLSNCCSSP WVN HIT QKLK SGETAANIAR ELAEQTRNHL NAGDITYS  
 AMDQLVGLLD VQLRNLT PGG KDSAARSLNK LQKRERSCRA YVQAMVETVN NLLQPQAL  
 WRDLTTS DQL RAATMLLDTV EESAFVLADN LLKTDIVREN TDNIQLEVAR LSTEGNLE  
 KFPENTGHGS TIQLSANTLK QNGRNGEIRV AFVLYNNLGP YLSTENASMK LGTEAMST  
 SVIVNSPVIT AAINKEFSNK VYLADPVVFT VKHIQSEEN FNPNCSEFSY SKRTMTGY  
 TQGCRLTTN KTHHTCSCNH LTNFAVLMAH VEVKHSDAVH DLLLDVITWV GILLSLVC  
 ICIFTFCFFR GLQSDRNTIH KNLCISLFVA ELLFLIGINR TDQPIACAVF AALLHFFF  
 AFTWMFLEGV QLYIMLVEVF ESEHSRRKYF YLVGYGMPAL IVAVSAAVDY RSYGTDKV  
 LRLDTYFIWS FIGPATLIIM LNVIFLGIAL YKMFHHTAIL KPESGCLDNI KSWVIGAI  
 LCLLGLTWAF GLMYINESTV IMAYLFTIFN SLQGMFIFIF HCVLQKKVRK EYGKCLRT  
 CSGKSTESSI GSGKTS GSRT PGRYSTGSQS RIRRMWNDTV RKQSESSFIT GDINSSAS  
 REGLLNNARD TSVMDTLP LN GNHGN SYSIA GGEYLSNCVQ IIDRGYNHNE TALEKKIL  
 LTSNYIPSYL NNHERSSEQN RNM MNKLVDN LGSGSEDDAI VLDDAASF NH EESLGLEL  
 EESDAPLLPP RYSTDNHQP HHYSRRRLPQ DHSESF FPLL TDEHTEDPQS PHRDSLYT  
 PALAGVPAAD SVTTSTQTEA AAAKG GDAED VYKSM PN LG SRNHVHPLHA YYQLGRGS  
 GFIVPPNKDG ASPEGTSKGP AHLVTSL

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